

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/736,936A  
Source: 1 Fw/b  
Date Processed by STIC: 7/27/00

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 07/27/2006

PATENT APPLICATION: US/10/736,936A

TIME: 10:32:16

Input Set : A:\Amended\_SL.ST25.txt

Output Set : N:\CRF4\07272006\J736936A.raw

3 <110> APPLICANT: Bristol-Myers Squibb Company  
 5 <120> TITLE OF INVENTION: Novel Organic Anion Transport Proteins  
 7 <130> FILE REFERENCE: DB23 DIV1  
 9 <140> CURRENT APPLICATION NUMBER: US 10/736,936A  
 10 <141> CURRENT FILING DATE: 2003-12-16  
 12 <150> PRIOR APPLICATION NUMBER: US 09/575,081  
 13 <151> PRIOR FILING DATE: 2000-05-19  
 15 <150> PRIOR APPLICATION NUMBER: US 60/135,081  
 16 <151> PRIOR FILING DATE: 1999-05-20  
 18 <160> NUMBER OF SEQ ID NOS: 29  
 20 <170> SOFTWARE: PatentIn version 3.2  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 2830  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (135)..(2207)  
 32 <400> SEQUENCE: 1

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35	attctaaatc caggtgattg tttcaaactg agcatcaaca acaaaaacat ttgtatgata	120
37	tctatatttc aatc atg gac caa aat caa cat ttg aat aaa aca gca gag	170
38	Met Asp Gln Asn Gln His Leu Asn Lys Thr Ala Glu	
39	1 5 10	
41	gca caa cct tca gag aat aag aaa aca aga tac tgc aat gga ttg aag	218
42	Ala Gln Pro Ser Glu Asn Lys Lys Thr Arg Tyr Cys Asn Gly Leu Lys	
43	15 20 25	
45	atg ttc ttg gca gct ctg tca ctc agc ttt att gct aag aca cta ggt	266
46	Met Phe Leu Ala Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly	
47	30 35 40	
49	gca att att atg aaa agt tcc atc att cat ata gaa cgg aga ttt gag	314
50	Ala Ile Ile Met Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu	
51	45 50 55 60	
53	ata tcc tct tct ctt gtt ggt ttt att gac gga agc ttt gaa att gga	362
54	Ile Ser Ser Ser Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly	
55	65 70 75	
57	aat ttg ctt gtg att gta ttt gtg agt tac ttt gga tcc aaa cta cat	410
58	Asn Leu Leu Val Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His	
59	80 85 90	
61	aga cca aag tta att gga atc ggt tgt ttc att atg gga att gga ggt	458
62	Arg Pro Lys Leu Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly	
63	95 100 105	
65	gtt ttg act gct ttg cca cat ttc ttc atg gga tat tac agg tat tct	506

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66 Val Leu Thr Ala Leu Pro His Phe Phe Met Gly Tyr Tyr Arg Tyr Ser
67      110                      115                      120
69 aaa gaa act aat atc gat tca tca gaa aat tca aca tcg acc tta tcc      554
70 Lys Glu Thr Asn Ile Asp Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser
71 125                      130                      135                      140
73 act tgt tta att aat caa att tta tca ctc aat aga gca tca cct gag      602
74 Thr Cys Leu Ile Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu
75      145                      150                      155
77 ata gtg gga aaa ggt tgt tta aag gaa tct ggg tca tac atg tgg ata      650
78 Ile Val Gly Lys Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile
79      160                      165                      170
81 tat gtg ttc atg ggt aat atg ctt cgt gga ata ggg gag act ccc ata      698
82 Tyr Val Phe Met Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile
83      175                      180                      185
85 gta cca ttg ggg ctt tct tac att gat gat ttc gct aaa gaa gga cat      746
86 Val Pro Leu Gly Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His
87      190                      195                      200
89 tct tct ttg tat tta ggt ata ttg aat gca ata gca atg att ggt cca      794
90 Ser Ser Leu Tyr Leu Gly Ile Leu Asn Ala Ile Ala Met Ile Gly Pro
91 205                      210                      215                      220
93 atc att ggc ttt acc ctg gga tct ctg ttt tct aaa atg tac gtg gat      842
94 Ile Ile Gly Phe Thr Leu Gly Ser Leu Phe Ser Lys Met Tyr Val Asp
95      225                      230                      235
97 att gga tat gta gat cta agc act atc agg ata act cct act gat tct      890
98 Ile Gly Tyr Val Asp Leu Ser Thr Ile Arg Ile Thr Pro Thr Asp Ser
99      240                      245                      250
101 cga tgg gtt gga gct tgg tgg ctt aat ttc ctt gtg tct gga cta ttc      938
102 Arg Trp Val Gly Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe
103      255                      260                      265
105 tcc att att tct tcc ata cca ttc ttt ttc ttg ccc caa act cca aat      986
106 Ser Ile Ile Ser Ser Ile Pro Phe Phe Phe Leu Pro Gln Thr Pro Asn
107      270                      275                      280
109 aaa cca caa aaa gaa aga aaa gct tca ctg tct ttg cat gtg ctg gaa      1034
110 Lys Pro Gln Lys Glu Arg Lys Ala Ser Leu Ser Leu His Val Leu Glu
111 285                      290                      295                      300
113 aca aat gat gaa aag gat caa aca gct aat ttg acc aat caa gga aaa      1082
114 Thr Asn Asp Glu Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys
115      305                      310                      315
117 aat att acc aaa aat gtg act ggt ttt ttc cag tct ttt aaa agc atc      1130
118 Asn Ile Thr Lys Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile
119      320                      325                      330
121 ctt act aat ccc ctg tat gtt atg ttt gtg ctt ttg acg ttg tta caa      1178
122 Leu Thr Asn Pro Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln
123      335                      340                      345
125 gta agc agc tat att ggt gct ttt act tat gtc ttc aaa tac gta gag      1226
126 Val Ser Ser Tyr Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu
127      350                      355                      360
129 caa cag tat ggt cag cct tca tct aag gct aac atc tta ttg gga gtc      1274
130 Gln Gln Tyr Gly Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val

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131	365		370		375		380	
133	ata acc ata cct att ttt gca agt gga atg ttt tta gga gga tat atc	1322						
134	Ile Thr Ile Pro Ile Phe Ala Ser Gly Met Phe Leu Gly Gly Tyr Ile							
135		385		390		395		
137	att aaa aaa ttc aaa ctg aac acc gtt gga att gcc aaa ttc tca tgt	1370						
138	Ile Lys Lys Phe Lys Leu Asn Thr Val Gly Ile Ala Lys Phe Ser Cys							
139		400		405		410		
141	ttt act gct gtg atg tca ttg tcc ttt tac cta tta tat ttt ttc ata	1418						
142	Phe Thr Ala Val Met Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile							
143		415		420		425		
145	ctc tgt gaa aac aaa tca gtt gcc gga cta acc atg acc tat gat gga	1466						
146	Leu Cys Glu Asn Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly							
147		430		435		440		
149	aat aat cca gtg aca tct cat aga gat gta cca ctt tct tat tgc aac	1514						
150	Asn Asn Pro Val Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn							
151	445		450		455		460	
153	tca gac tgc aat tgt gat gaa agt caa tgg gaa cca gtc tgt gga aac	1562						
154	Ser Asp Cys Asn Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn							
155		465		470		475		
157	aat gga ata act tac atc tca ccc tgt cta gca ggt tgc aaa tct tca	1610						
158	Asn Gly Ile Thr Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser							
159		480		485		490		
161	agt ggc aat aaa aag cct ata gtg ttt tac aac tgc agt tgt ttg gaa	1658						
162	Ser Gly Asn Lys Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu							
163		495		500		505		
165	gta act ggt ctc cag aac aga aat tac tca gcc cat ttg ggt gaa tgc	1706						
166	Val Thr Gly Leu Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys							
167		510		515		520		
169	cca aga gat gat gct tgt aca agg aaa ttt tac ttt ttt gtt gca ata	1754						
170	Pro Arg Asp Asp Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile							
171	525		530		535		540	
173	caa gtc ttg aat tta ttt ttc tct gca ctt gga ggc acc tca cat gtc	1802						
174	Gln Val Leu Asn Leu Phe Phe Ser Ala Leu Gly Gly Thr Ser His Val							
175		545		550		555		
177	atg ctg att gtt aaa att gtt caa cct gaa ttg aaa tca ctt gca ctg	1850						
178	Met Leu Ile Val Lys Ile Val Gln Pro Glu Leu Lys Ser Leu Ala Leu							
179		560		565		570		
181	ggt ttc cac tca atg gtt ata cga gca cta gga gga att cta gct cca	1898						
182	Gly Phe His Ser Met Val Ile Arg Ala Leu Gly Gly Ile Leu Ala Pro							
183		575		580		585		
185	ata tat ttt ggg gct ctg att gat aca acg tgt ata aag tgg tcc acc	1946						
186	Ile Tyr Phe Gly Ala Leu Ile Asp Thr Thr Cys Ile Lys Trp Ser Thr							
187		590		595		600		
189	aac aac tgt ggc aca cgt ggg tca tgt agg aca tat aat tcc aca tca	1994						
190	Asn Asn Cys Gly Thr Arg Gly Ser Cys Arg Thr Tyr Asn Ser Thr Ser							
191	605		610		615		620	
193	ttt tca agg gtc tac ttg ggc ttg tct tca atg tta aga gtc tca tca	2042						
194	Phe Ser Arg Val Tyr Leu Gly Leu Ser Ser Met Leu Arg Val Ser Ser							
195		625		630		635		

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197 ctt gtt tta tat att ata tta att tat gcc atg aag aaa aaa tat caa      2090
198 Leu Val Leu Tyr Ile Ile Leu Ile Tyr Ala Met Lys Lys Lys Tyr Gln
199          640          645          650
201 gag aaa gat atc aat gca tca gaa aat gga agt gtc atg gat gaa gca      2138
202 Glu Lys Asp Ile Asn Ala Ser Glu Asn Gly Ser Val Met Asp Glu Ala
203          655          660          665
205 aac tta gaa tcc tta aat aaa aat aaa cat ttt gtc cct tct gct ggg      2186
206 Asn Leu Glu Ser Leu Asn Lys Asn Lys His Phe Val Pro Ser Ala Gly
207          670          675          680
209 gca gat agt gaa aca cat tgt taaggggaga aaaaaagcca cttctgcttc      2237
210 Ala Asp Ser Glu Thr His Cys
211 685          690
213 tgtgtttcca aacagcattg cattgattca gtaagatgtt atttttgagg agttcctggt      2297
215 cctttcacta agaatttcca catcttttat ggtggaagta taaataagcc tatgaactta      2357
217 taataaaaca aactgtagggt agaaaaaatg agagtactca ttgttacatt atagctacat      2417
219 atttgtgggt aagggttagac tatatgatcc atacaaatta aagtgaagaga catgggttact      2477
221 gtgtaataaa agaaaaaata cttgttcagg taattctaatt tcttaataaa acaaatgagt      2537
223 atcatacagg tagagggttaa aaaggaggag ctagattcat atcctaagta aagagaaatg      2597
225 cctagtgtct attttattaa acaaacaac acagagtttg aactataata ctaaggcctg      2657
227 aagtctagct tggatatatg ctacaataat atctgttact cacataaaat tatatatattc      2717
229 acagacttta tcaatgtata attaacaatt atcttgttta agtaaattta gaatacattt      2777
231 aagtattgtg gaagaaataa agacattcca atatttgcaa aaaaaaaaaa aaa      2830
234 <210> SEQ ID NO: 2
235 <211> LENGTH: 691
236 <212> TYPE: PRT
237 <213> ORGANISM: Homo sapiens
239 <400> SEQUENCE: 2
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245 Glu Asn Lys Lys Thr Arg Tyr Cys Asn Gly Leu Lys Met Phe Leu Ala
246          20          25          30
249 Ala Leu Ser Leu Ser Phe Ile Ala Lys Thr Leu Gly Ala Ile Ile Met
250          35          40          45
253 Lys Ser Ser Ile Ile His Ile Glu Arg Arg Phe Glu Ile Ser Ser Ser
254          50          55          60
257 Leu Val Gly Phe Ile Asp Gly Ser Phe Glu Ile Gly Asn Leu Leu Val
258 65          70          75          80
261 Ile Val Phe Val Ser Tyr Phe Gly Ser Lys Leu His Arg Pro Lys Leu
262          85          90          95
265 Ile Gly Ile Gly Cys Phe Ile Met Gly Ile Gly Gly Val Leu Thr Ala
266          100         105         110
269 Leu Pro His Phe Phe Met Gly Tyr Tyr Arg Tyr Ser Lys Glu Thr Asn
270          115         120         125
273 Ile Asp Ser Ser Glu Asn Ser Thr Ser Thr Leu Ser Thr Cys Leu Ile
274          130         135         140
277 Asn Gln Ile Leu Ser Leu Asn Arg Ala Ser Pro Glu Ile Val Gly Lys
278 145         150         155         160
281 Gly Cys Leu Lys Glu Ser Gly Ser Tyr Met Trp Ile Tyr Val Phe Met
282          165         170         175

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285 Gly Asn Met Leu Arg Gly Ile Gly Glu Thr Pro Ile Val Pro Leu Gly
286      180      185      190
289 Leu Ser Tyr Ile Asp Asp Phe Ala Lys Glu Gly His Ser Ser Leu Tyr
290      195      200      205
293 Leu Gly Ile Leu Asn Ala Ile Ala Met Ile Gly Pro Ile Ile Gly Phe
294      210      215      220
297 Thr Leu Gly Ser Leu Phe Ser Lys Met Tyr Val Asp Ile Gly Tyr Val
298 225      230      235      240
301 Asp Leu Ser Thr Ile Arg Ile Thr Pro Thr Asp Ser Arg Trp Val Gly
302      245      250      255
305 Ala Trp Trp Leu Asn Phe Leu Val Ser Gly Leu Phe Ser Ile Ile Ser
306      260      265      270
309 Ser Ile Pro Phe Phe Phe Leu Pro Gln Thr Pro Asn Lys Pro Gln Lys
310      275      280      285
313 Glu Arg Lys Ala Ser Leu Ser Leu His Val Leu Glu Thr Asn Asp Glu
314      290      295      300
317 Lys Asp Gln Thr Ala Asn Leu Thr Asn Gln Gly Lys Asn Ile Thr Lys
318 305      310      315      320
321 Asn Val Thr Gly Phe Phe Gln Ser Phe Lys Ser Ile Leu Thr Asn Pro
322      325      330      335
325 Leu Tyr Val Met Phe Val Leu Leu Thr Leu Leu Gln Val Ser Ser Tyr
326      340      345      350
329 Ile Gly Ala Phe Thr Tyr Val Phe Lys Tyr Val Glu Gln Gln Tyr Gly
330      355      360      365
333 Gln Pro Ser Ser Lys Ala Asn Ile Leu Leu Gly Val Ile Thr Ile Pro
334      370      375      380
337 Ile Phe Ala Ser Gly Met Phe Leu Gly Gly Tyr Ile Ile Lys Lys Phe
338 385      390      395      400
341 Lys Leu Asn Thr Val Gly Ile Ala Lys Phe Ser Cys Phe Thr Ala Val
342      405      410      415
345 Met Ser Leu Ser Phe Tyr Leu Leu Tyr Phe Phe Ile Leu Cys Glu Asn
346      420      425      430
349 Lys Ser Val Ala Gly Leu Thr Met Thr Tyr Asp Gly Asn Asn Pro Val
350      435      440      445
353 Thr Ser His Arg Asp Val Pro Leu Ser Tyr Cys Asn Ser Asp Cys Asn
354      450      455      460
357 Cys Asp Glu Ser Gln Trp Glu Pro Val Cys Gly Asn Asn Gly Ile Thr
358 465      470      475      480
361 Tyr Ile Ser Pro Cys Leu Ala Gly Cys Lys Ser Ser Ser Gly Asn Lys
362      485      490      495
365 Lys Pro Ile Val Phe Tyr Asn Cys Ser Cys Leu Glu Val Thr Gly Leu
366      500      505      510
369 Gln Asn Arg Asn Tyr Ser Ala His Leu Gly Glu Cys Pro Arg Asp Asp
370      515      520      525
373 Ala Cys Thr Arg Lys Phe Tyr Phe Phe Val Ala Ile Gln Val Leu Asn
374      530      535      540
377 Leu Phe Phe Ser Ala Leu Gly Gly Thr Ser His Val Met Leu Ile Val
378 545      550      555      560
381 Lys Ile Val Gln Pro Glu Leu Lys Ser Leu Ala Leu Gly Phe His Ser

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; Xaa Pos. 33,594

Seq#:8; Xaa Pos. 33,594

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:29

**VERIFICATION SUMMARY**

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L:1241 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:748  
L:1381 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:2428  
L:1492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:32  
L:1632 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:592